

Claims with Markings to Show Changes

At page 1, delete the third paragraph (lines 12-14).

At page 1, line 5, before "Statement" insert the following paragraph:

Reference to Related Applications.

This application is a continuation-in-part of PCT/US98/10080, filed May 15, 1998, which is a continuation-in-part of U.S.S.N. 08/888,534, filed July 7, 1997, and U.S.S.N. 08/857,076, filed May 15, 1997, issued as U.S. Patent No. 6,225,120 on May 1, 2001.

At page 83, replace the second paragraph (lines 14-26) with the following replacement paragraph:

Score = 151 (68.4 bits), Expect = $1.9e-140$, Sum P(8) = $1.9e-140$
Identities = 28/54 (51%), Positives = 38/54 (70%)

SEQ ID NO: 161 AFX:226 SPVGHFAKWSGSPCSRNRREADMWTTFRPRSSSNASSVSTRLSPLRPSEVLAE279
SEQ ID NO: 162 SP F+KW SP S + ++ D W+TFRPR+SSNAS++S RLSP+ E + L E
SEQ ID NO: 163 FKHR:287 SPGSQFSKWPASPGSHSNDDFDNWSTFRPRTSSNASTISGRLSPIMTEQDDLGE340
SEQ ID NO: 164 DAF-16a SFRPRTQSNLSIPGSSS

Score = 132 (59.8 bits), Expect = $1.9e-140$, Sum P(8) = $1.9e-140$
Identities = 22/42 (52%), Positives = 28/42 (66%)

SEQ ID NO: 165: AFX: 7 KAAAIIDLDPDFEPQSRPRSCTWPLPRPEIANQPSEPPEVEP 48
SEQ ID NO: 166 +A+++DPD FEP RPRSCTWPLPRPE + S P
SEQ ID NO: 167 FKHR: 3 EAPQVVEIDPDFEPLPRPRSCTWPLPRPEFSQNSATSSPAP 44
SEQ ID NO: 168 DAF-16 TFMNTPDDVMMNDDMEPIPRDRCNTWPMRRPQLEPPLNSSP 177
SEQ ID NO: 169 T ++P+ V ++ D EP+PR R TWP+ RP++ + +++++

Beginning at page 97, please replace page 97, second paragraph (lines 3-37), page 98, page 99, and page 100, first paragraph (lines 1-4) with the following replacement paragraphs.

Score = 252 (88.7 bits), Expect = 2.2e-60, Sum P(6) = 2.2e-60
Identities = 47/80 (58%), Positives = 60/80 (75%), Frame = +3

SEQ ID NO:170 Query:439 LEKQAGGNPWHQFVENNLILKMGPVDKRGKFARRRQLLLTGEPHLYYVDPVNKVLKGEI 498
SEQ ID NO:171 LE+Q NP+H F N+LILK G ++K++GLFARRR LLTEGPHL Y+D N VLKGE+
SEQ ID NO:172 Sbjct:1818 LEEQRVKNPFFHIFTNNSLILKQGYLEKKRGKFARRRMFLLTGEPHLLYIDVPNVLKGEV1997

SEQ ID NO:170 Query: 499 PWSQELRPEAKNFKTFVHT 518
SEQ ID NO:171 PW+ ++ E KN TFF+HT
SEQ ID NO:172 Sbjct: 1998 PWTPCMQVELKNSGTFFIHT 2057

Score = 201 (70.8 bits), Expect = 2.2e-60, Sum P(6) = 2.2e-60
Identities = 48/123 (39%), Positives = 72/123 (58%), Frame = +1

SEQ ID NO:173 Query: 263 SDLWALGCIIYQLVAGLPPFRAGNEYLIFQKIIKLEYDFPEKFFPKARDLVEKLLVL DAT 322
SEQ ID NO:174 +D+W LGCI++Q +AG PPFRA N+Y + ++I +L++ FPE F +A +++ K+LV
SEQ ID NO:175 Sbjct: 802 TDIWGLGCILFQCLAGQPFRVAVNQYHLLKRIQELDFSFPPEGFPPEASEIIAKILV--G*H 978

SEQ ID NO:173 Query: 323 KRLGCE----EMEGYGP-----LKAHPFFESVTWENLHQQTTPPKLTAYLPAMSEDDE 370
SEQ ID NO:174 + L E ++ P L AH FFE+V W N+ PP L AY+PA + E
SEQ ID NO:175 Sbjct: 979 ETLKTEYVIFNLQVRDPSTRITSQELMAHKFFENVDWVNIANIKPPVLHAYIPATFGEPE1158

SEQ ID NO:173 Query: 371 DCYGN 375
SEQ ID NO:174 Y N
SEQ ID NO:175 Sbjct: 1159 -YYSN 1170

Score = 180 (63.4 bits), Expect = 2.2e-60, Sum P(6) = 2.2e-60
Identities = 31/72 (43%), Positives = 52/72 (72%), Frame = +2

SEQ ID NO:176 Query: 157 FGLSYAKNGELLKYIRKIGSFDECTRFYTAEIVSALEYLHGKGIHRDLKPENILLNED 216
SEQ ID NO:177 F + +NG+L + + GSFD ++F+ +EI++ L++LH I+HRD+KP+N+L+ +D
SEQ ID NO:178 Sbjct: 287 FVIGLVENGDLGESLCHFGSFDMLTSKFFASEILTGLQFLHDNKIVHRDMKPDNVL IQD 466

SEQ ID NO:176 Query: 217 MHIQITDFGTAK 228
SEQ ID NO:177 HI ITDFG+A+
SEQ ID NO:178Sbjct: 467 GHILITDFGSAQ 502

Score = 83 (29.2 bits), Expect = 2.2e-60, Sum P(6) = 2.2e-60
Identities = 15/53 (28%), Positives = 32/53 (60%), Frame = +

SEQ ID NO:179 Query:108 YAIKILEKRHIKENKVPYVTRERDVMSRLD----HPFFVKLYFTFQDDEKL 155
SEQ ID NO:180 +A+K+L+K ++ + K+ + RE++++ L HPF +LY F D ++
SEQ ID NO:181 Sbjct: 8 FAVKVLQKSYLNRHQMDAIIREKNILTYLSQECGGHPFVTQLYTHFHDQARI 166

Score = 81 (28.5 bits), Expect = 2.2e-60, Sum P(6) = 2.2e-60
Identities = 15/29 (51%), Positives = 19/29 (65%), Frame = +2

SEQ ID NO:182 Query: 519 PNRTYYLMDPSGNAHKWCRKIQEVWRQRY 547
SEQ ID NO:183 PNR YYL D A +WC+ I +V R+RY
SEQ ID NO:184 Sbjct: 2129 PNRVYYLFDLEKKADEWCKAINDV-RKRY 2212

Score = 78 (27.5 bits), Expect = 2.2e-60, Sum P(6) = 2.2e-60
Identities = 15/25 (60%), Positives = 18/25 (72%), Frame = +3

SEQ ID NO:185 Query: 232 PESKQARANSFVGTAQYVSPPELLTE 256
SEQ ID NO:186 PE AR +FVGTA YVSPE+L +
SEQ ID NO:187 Sbjct: 660 PEENTARRTTFVGTALYVSPEMLAD 734

Overall, *C. elegans* *pdk-1* exhibits the following homology to human PDK-1.

Score = 118 (54.4 bits), Expect = 1.4e-104, Sum P(5) = 1.4e-104
Identities = 21/62 (33%), Positives = 41/62 (66%)

SEQ ID NO:188 Query: 63 KRTSNDFMFLQSMGEGAYSQVFRCEVATDAMFAVKVLQKSYLNRHQKMDAIIREKNILT 122
SEQ ID NO:189 K+ DF F + +GEG++S V RE+AT +A+K+L+K ++ + K+ + RE+++++
SEQ ID NO:190 Sbjct: 76 KKRPEDFKFGKILGEGSFSTVVLARELATSREYAIIKILEKRHIKENKVPYVTRERDVMS 135

SEQ ID NO:188 Query: 123 YL 124
SEQ ID NO:189 L
SEQ ID NO:190 Sbjct: 136 RL 137

Score = 230 (106.0 bits), Expect = 1.4e-104, Sum P(5) = 1.4e-104
Identities = 39/90 (43%), Positives = 63/90 (70%)

SEQ ID NO:191 Query: 131 HPFVTQLYTHFDQARIYFVIGLVENGDLGESLCHFGSFDMLTSKFFASEILTGLQFLHD 190
SEQ ID NO:192 HPF +LY F D ++YF + +NG+L + + GSFD ++F+ +EI++ L++LH
SEQ ID NO:193 Sbjct: 139 HPFFVKLYFTFQDDEKLYFGLSYAKNGELLKYIRKIGSFDECTRFYTAEIVSALEYLHG 198

SEQ ID NO:191 Query: NKIVHRDMKPDNVLIQKDGHILITDFGSAQ 220
SEQ ID NO:192 I+HRD+KP+N+L+ +D HI ITDFG+A+
SEQ ID NO:193 Sbjct: KGIIHRDLKPENILLNEDMHIQITDFGTAK 228

Score = 238 (109.7 bits), Expect = 1.4e-104, Sum P(5) = 1.4e-104
Identities = 43/98 (43%), Positives = 67/98 (68%)

SEQ ID NO:194 Query: 259 EENTARRTTFVGTALYVSPEMLADGDVGPDQTDIWLGLCILFQCLAGQPPFRAVNQYHLK 318
SEQ ID NO:195 E AR +FVGTA YVSPE+L + +D+W LGCI++Q +AG PPFRA N+Y + +
SEQ ID NO:196 Sbjct: 233 ESKQARANSFVGTAQYVSPPELLTEKSACKSSDLWALGCIYQLVAGLPPFRAGNEYLIFQ 292

SEQ ID NO:194 Query: 319 RIQELDFSFPPEGFPPEEASEIIAKILVRDPSTRITSQEL 356
SEQ ID NO:195 +I +L++ FPE F +A +++ K+LV D + R+ +E+
SEQ ID NO:196 Sbjct: 293 KIIKLEYDFPEKFFPKARDLVEKLLVLVDATKRLGCEEM 330

Score = 85 (39.2 bits), Expect = 1.4e-104, Sum P(5) = 1.4e-104
Identities = 17/35 (48%), Positives = 21/35 (60%)

SEQ ID NO:197 Query: 356 LMAHKFFENVVDWVNIANIKPPVLHAYIPATFGEPE 390
SEQ ID NO:198 L AH FFE+V W N+ PP L AY+PA + E
SEQ ID NO:199 Sbjct: 336 LKAHPFFESVTWENLHQQTTPPKLTAYLPAMSEDDE 370

Score = 324 (149.3 bits), Expect = 1.4e-104, Sum P(5) = 1.4e-104
Identities = 59/104 (56%), Positives = 75/104 (72%)

SEQ ID NO:200 Query: 458 LEEQRVKNPFIHFTNNSLILKQGYLEKKRGLFARRRMFLLTGPHLLYIDVPNLVLKGEV 517
SEQ ID NO:201 LE+Q NP+H F N+LILK G ++K++GLFARRR LLTEGPHL Y+D N VLKGE+

SEQ ID NO:202 Sbjct: 439 LEKQAGGNPWHQFVENNLILKMGPVDRKGLFARRRQLLLTEGPHLYYVDPVNKVLKGEI 498

SEQ ID NO:200 Query: 518 PWTPCMQVELKNSGTFIFIHTPNRVYYLFDLEKKADEWCKAINDV 561

SEQ ID NO:201 PW+ ++ E KN TFF+HTPNR YYL D A +WC+ I +V

SEQ ID NO:202 Sbjct: 499 PWSQELRPEAKNFKTFVHTPNRTYYLMDPSGNAHKWCRKIQEV 542

Mapping of the *mg142* mutation to this open reading frame establishes the function of this protein. It is much more closely related to PDK than to any other known kinase. PDK is a mammalian kinase that phosphorylates an essential serine residue on AKT, contributing to its activation. The region of *akt-1* phosphorylated by PDK-1 is shown below (SEQ ID NO: 203-207, and 305).

SEQ ID NO:203 human AKT 276 KLENLMLDKDGHIKITDFGLCKEGIKDGATMKTFCGTPEYLAPEV 320

SEQ ID NO:204 KLENL+LDKDGHIKI DFGLCKE I G TFCGTPEYLAPEV

SEQ ID NO:205 Ce akt-1 33509 KLENLLLDKDGHIKIADFGLCKEISFGDKTSTFCGTPEYLAPEV 33643

SEQ ID NO:206 Ceakt2 326 LCKEEIKYDKTSTFCGTPEYLAPEVIEDIDYDRSVDWWGVGVVYEMMCGRLPFSKENGK

SEQ ID NO:207 LCKE I G TFCGTPEYLAPEV+ED DYR+VDWWG+GVVYEMMCGRLPF +++ +

SEQ ID NO:305 moAKT: 298 LCKEGISDGATMKTFCGTPEYLAPEVLEDNDYGRAVDWWGLGVVYEMMCGRLPFYNQDHER

Replace page 178, fourth paragraph, lines 21-24, page 179-186, and page 187, first paragraph, lines 1-14, with the following replacement paragraphs:

Pepck

>R11A5

Length = 26,671

Plus Strand HSPs:

Score = 994 (461.5 bits), Expect = 0.0, Sum P(5) = 0.0

Identities = 176/223 (78%), Positives = 195/223 (87%), Frame = +1

SEQ ID NO:211 Query:201 AKNNGEFVRCVHSVGPQPKPVATKVINHWPCNPEKTIIAHRPAEREIWSFGSGYGGNSLLG 260

SEQ ID NO:212 A N +FVRC+HSVG P+PV +VINHWPCNPE+ +IAHRP EREIWSFGSGYGGNSLLG

SEQ ID NO:213Sbjct:8682 ALGNQDFVRCIHSVGLPRPVKQVRVINHWPCNPERVLIARPPEREIWSFGSGYGGNSLLG 18861

SEQ ID NO:211 Query: 261 KKCFFALRIAMNIGYDEGWMAEHMLIMGVTS PKGEERFVAAAFPSACGKTNLAMLEPTIPG 320

SEQ ID NO:212 KKCFFALRIA NI DEGWMAEHMLIMGV T P G E F+AAAFPSACGKTNLAMLEPT+PG

SEQ ID NO:213 Sbjct:18862 KKCFFALRIASNIAKDEGWMAEHMLIMGVTRPCGREHFIAAFPSACGKTNLAMLEPTLPG 19041

SEQ ID NO:211 Query: 321 WKVRVIGDDIAWMKFGADGRLYAINPEYGFVGVPAGTSHKTNPMAMASFQENTIFTNVAE 380

SEQ ID NO:212 WKVR +GDDIAWMKFG DGRLYAINPE GFFGVAPGTS+KTNPMA+A+FQ+N+IFTNVAE

SEQ ID NO:213 Sbjct:19042 WKVRCVGDDIAWMKFGEDGRLYAINPEAGFFGVAPGTSNKTNPMAVATFQKNSIFTNVAE 19221

SEQ ID NO:211 Query: 381 TADGEYFWEGLEHEVKNPKVDMINWLGEPPWHIGDESKAAHPNS 423

SEQ ID NO:212 TA+GEYFWEGLE E+ + VD+ WLGE WHIG+ AAHPNS

SEQ ID NO:213 Sbjct: 19222 TANGEYFWEGLEDEIADKNVDITTLWGEKWHIGEPGVAAHPNS 19350

Score = 657 (305.1 bits), Expect = 0.0, Sum P(5) = 0.0

Identities = 120/173 (69%), Positives = 144/173 (83%), Frame = +1

SEQ ID NO:214 Query: 32 KGDFVSLPKHVQRFVAEKAELMKPSAIFICDGSQNEADELIARCVLPLKAYKNNY 91
 SEQ ID NO:215 +GDF LP VQRF+AEKAELM+P IFICDGSQ+EADELI + +ERG+L L+AY+NNY
 SEQ ID NO:216 Sbjet:18181 QGDFHLLPAKVQRFIAEKAELMRPRGIFICDGSQHEADELIDKLIERGMLSKLEAYENNY 18360

SEQ ID NO:214 Query: 92 LCRTDPRDVARVESKTWMITPEKYDSVCHTPEGVKPMMGQWMSPEFGKELDDRFPGCMA 151
 SEQ ID NO:215 +CRTDP+DVARVESKTWM+T KYD+V HT EGV+P+MG W++P++ ELD RFPGCMA
 SEQ ID NO:216 Sbjet:18361LCRTDPKDVARVESKTWMVTKNKYDTVTHTKEGVPEIMGHWLAPEDLATELDSRFPGCMA 18540

SEQ ID NO:214 Query: 152 GRTMYVIPYSMPGVGGPLSKIGIELTDSYVVLICMRIMTRMGEPVLKALAKNN 204
 SEQ ID NO:215 GR MYVIP+SMGPVGGPLSKIGI+LTDS+YVVL MRIMTR+ V AL +
 SEQ ID NO:216 Sbjet: 18541 GRIMYVIPFSMPGVGGPLSKIGIQLTDSNYVVLMSRIMTRVNDVWDALGNQD 18699

Score = 453 (210.3 bits), Expect = 0.0, Sum P(5) = 0.0
 Identities = 77/107 (71%), Positives = 90/107 (84%), Frame = +1

SEQ ID NO:217 Query: 424 RFTAPAGQCPIIHPDWEKPEGVPIDAIIFGGRRPEGVPLVFESRSWVHGIFVGACVKSEA 483
 SEQ ID NO:218 RF APA QCPIIHPDWE P+GVPI+AIIFGGRRP+GVPL++E+ SW HG+F G+C+KSEA
 SEQ ID NO:219 Sbjet:19396 RFAAPANQCPIIHPDWE PQGVPIEAIIFGGRRPQGVPLIYETNSWEHGVFTGSCCLKSEA 19575

SEQ ID NO:217 Query: 484 TAAAEHTGKQVMHDPAMRPFMGYNFGRYMRHWMKLGQPPHKVPKIF 530
 SEQ ID NO:218 TAAAE TKG VMHDPAMRPFMGYNFG+Y++HW+ L KV F
 SEQ ID NO:219 Sbjet: 19576 TAAAEFTGKTMHDPAMRPFMGYNFGKYLQHWLCLKTDSRKVIDFF 19716

Score = 404 (187.6 bits), Expect = 0.0, Sum P(5) = 0.0
 Identities = 68/116 (58%), Positives = 89/116 (76%), Frame = +1

SEQ ID NO:220 Query: 526 VPKIFHVNWFRQSADHKFLWPYGDNIRVIDWILRRCSGDATIAEETPIGFIPKKGITINL585
 SEQ ID NO:221 +PKI+HVNWFR+ +++KFLWPG+GDNIRVIDWI+RR G+ I ETPIG +P KG+INL
 SEQ ID NO:222 Sbjet: 19750 MPKIYHVNWFRKDSNNKFLWPGFGDNIRVIDWIIRRLDGEQEIGVETPIGTVPAKGSINL 19929

SEQ ID NO:220 Query: 586 EGLPNVNWDELMSIPKSYWLEDVMVETKTFFENQVGSDDLPEIAKELEAQTERIKAL 641
 SEQ ID NO:221 EGL VNWDELMS+P YW +D E + F + QVG DLP + E++AQ +R++ L
 SEQ ID NO:222 Sbjet: 19930 EGLGEVNWDELMSVPADYWKQDAQEIRKFLDEQVGEDLPEPVRAEMDAQEKRVQTL 20097

Score = 69 (32.0 bits), Expect = 0.0, Sum P(5) = 0.0
 Identities = 15/36 (41%), Positives = 21/36 (58%), Frame = +1

SEQ ID NO:223 Query: 5 SLSHFKDDDFAVVSEVVTHKQNHIPVIKGVSLPK 40
 SEQ ID NO:224 SL +D F VV+EVV + H+P++K F S K
 SEQ ID NO:225 Sbjet: 14722 SLRQISEDAFYVNVNEVVMKRLGHVPILKVIFESSEK 14829

Score = 39 (18.1 bits), Expect = 6.9e-244, Sum P(4) = 6.9e-244
 Identities = 9/25 (36%), Positives = 11/25 (44%), Frame = +3

SEQ ID NO:226 Query: 148 GCMAGRTMYVIPYSMPGVGGPLSKI 172
 SEQ ID NO:227 GC R + V P S PL K+
 SEQ ID NO:228 Sbjet: 8040 GCSGRRVLCVPCSHSSSALPLQKV 8114

Score = 38 (17.6 bits), Expect = 4.0e-285, Sum P(5) = 4.0e-285
 Identities = 7/16 (43%), Positives = 9/16 (56%), Frame = +1

SEQ ID NO:229 Query: 588 LPNVNWDELMSIPKSY 603
 SEQ ID NO:230 L + NW +S P SY
 SEQ ID NO:231 Sbjet: 22654 LESFNWFSFVSCPSY 22701

Score = 37 (17.2 bits), Expect = 2.0e-48, Sum P(3) = 2.0e-48
 Identities = 6/14 (42%), Positives = 9/14 (64%), Frame = +1

SEQ ID NO:232 Query: 117 SVCHTPEGVKPMMG 130

SEQ ID NO:233 +V H P ++P MG
SEQ ID NO:234 Sbjct: 19603 TVMHDPMAMRPFMG 19644

Acetyl coa carboxylase

>W09B6

Length = 32,900

Plus Strand HSPs:

Score = 562 (259.1 bits), Expect = 0.0, Sum P(14) = 0.0
Identities = 109/197 (55%), Positives = 138/197 (70%), Frame = +2

SEQ ID NO:235 Query: 1951 SGFFDYGSFSEIMQPWQAQTVVVGRRARLGGIPVGVVAVETRTVELSVPADPANLDSEAKII 2010
SEQ ID NO:236 z +G D SF EI WA+++V GRARL GIP+GVV+ E R VPADPA S+ +
SEQ ID NO:237 Sbjct:28280 TGICDTMSFDEICGDWAKSIVAGRARLCGIPIGVVSSEFRNFSTIVPADPAIDGSQVQNT 28459

SEQ ID NO:235 Query: 2011 QQAGQVWFPSAFKTYQAIKDFNREGLPLMVFANWRGFSGGMKDMYDQVLKFGAYIVDGL 2070
SEQ ID NO:236 Q+AGQVW+PDSAFKT +AI D N+E LPLM+ A+ RGFSGG KDMYD VLKFGA IVD L
SEQ ID NO:237 Sbjct:28460 QRAGQVWYPDSAFKTAEAINDLNKENLPLMIASLRGFSGGQKDMYDMVLKFGAQIVDAL 28639

SEQ ID NO:235 Query: 2071 RECSQPMVMYIPQAEALRGSSWVIDPTINPRHMEMYADRESRGSVLEPEGTVEIKFRKK 2130
SEQ ID NO:236 ++PV+VYIP ELRGG+W V+D I P + + AD +SRG +LEP V IKFRK
SEQ ID NO:237 Sbjct: 28640 AVYNRPVIVYIPEAGELRGGAVALDSKIRPEFIHLVADEKSRGGILEPNAVVGIKFRKP 28819

SEQ ID NO:235 Query: 2131 DLVKTMRVDPVYIRLA 2147
SEQ ID NO:236 +++ M+R DP Y +L+
SEQ ID NO:237 Sbjct: 28820 MMEMMKRSDPTYSKLS 28870

Score = 357 (164.6 bits), Expect = 0.0, Sum P(14) = 0.0
Identities = 68/124 (54%), Positives = 89/124 (71%), Frame = +2

SEQ ID NO:238 Query:303 VGYPVMIKASEGGGGKGIRKVNADDFPNLFRQVQAEVPGSPIFVMRLAKQSRHLEVQIL 362
SEQ ID NO:239 +G+P+MIKASEGGGGKGIRK +DF ++F +V EV GSPIF+M+ +RH+EVQ+L
SEQ ID NO:240 Sbjct:23264IGFPLMIKASEGGGGKGIRKCTKVEDFKSMFEEVAQEVQGSPIFLMKCVDGARHIEVQLL 23443

SEQ ID NO:238 Query: 363 ADQYGNALISLFRDCSVQRRHQKXXXXXXXXXXXXVFEHMEQCAVKLAKMVGYSAGTV 422
SEQ ID NO:239 AD+Y N IS++ RDQS+QRR QK + + M++ AV+LAK VGY SAGTV
SEQ ID NO:240 Sbjct:23444ADRYENVISVYTRDCSIQRRCKIIEEAPAIASSHIRKSMQEDAVRLAKYVGYESAGTV 23623

SEQ ID NO:238 Query: 423 EYLY 426
SEQ ID NO:239 EYLY
SEQ ID NO:240 Sbjct: 23624 EYLY 23635

Score = 345 (159.1 bits), Expect = 0.0, Sum P(14) = 0.0
Identities = 65/116 (56%), Positives = 86/116 (74%), Frame = +2

SEQ ID NO:241 Query:1787 KEEGLGAENLRGSGMIAGESSLAYDEIITISLVTCTRAIGIGAYLVRLGQRTIQVENSILI 1846
SEQ ID NO:242 K E +G ENL+GSG+IAGE++ AY E+ T VT R++GIGAY RL R +Q + SHLI
SEQ ID NO:243 Sbjct:27794 KNEKIGVENLQSGSLIAGETARAYAENVPTCYVTGRSVGIGAYTARLAHRIVQHKQSHLI 27973

SEQ ID NO:241 Query: 1847 LTGAGALNKVLGREVYTSNNQLGGIIMHNNGVTHCTVCDDFEGVFTVLHWLSYMP 1902
SEQ ID NO:242 LTG ALN +LG++VYTSNNQLGG ++M NGVTH V +D EG+ V+ W+S++P
SEQ ID NO:243 Sbjct: 27974 LTGYEALNTLLGKKVYTSNNQLGGPEVMFRNGVTHAVVDNDLEGIKAVIRWMSFLP 28141

Score = 319 (147.1 bits), Expect = 0.0, Sum P(14) = 0.0
Identities = 59/119 (49%), Positives = 80/119 (67%), Frame = +2

SEQ ID NO:244 Query: 503 HVIAARITSENPDGFKPSSGTVQELNFRSNKNVWGYFSVAAAGGLHEFADSQFGHCFWSW 562
SEQ ID NO:245 H IAARIT ENPD+ F+PS+G V E+NF S+++ W YFSV +H+FADSQFGH F+
SEQ ID NO:246 Sbjct:23870 HAIAARITCENPDDSFPRSTGKVEINFPSSQDAWAYFSVGRGSSVHQFADSQFGHIFTR 24049

SEQ ID NO:244 Query: 563 GENREEAISNMVVALKELSIRGDFRTTVEYLIKLETESFQLNRIDTGWLDRLIAEKVQ 621
SEQ ID NO:245 G +R EA++ M LK ++IR F T V YL+ L+ F N +T WLD+ IA K++
SEQ ID NO:246 Sbjct: 24050 GTSRTEAMNTMCSTLKHMTIRSSFPTQVNYLVLDLMDADFINNAFNTQWLDKRIAMKIK 24226

Score = 303 (139.7 bits), Expect = 0.0, Sum P(14) = 0.0
Identities = 55/90 (61%), Positives = 70/90 (77%), Frame = +2

SEQ ID NO: 247 Query: 178 PGGANNNNYANVELILDIARIPVQAVWAGWGHASENPKLPELLKNGIAFMGPPSQAMW 237
SEQ ID NO: 248 P G N NN+ANV+ IL A + V AVWAGWGHASEN LP L + IAF+GPP+ AM+
SEQ ID NO: 249 Sbjct: 22886 PSGTNKNNFANVDEILKHAIKYEYDAVWAGWGHASENPDLPRRLNDHNIAGFIPGPASAMF 23065

SEQ ID NO: 247 Query: 238 ALGDKIASSIVAQTAGIPTLPWSGSGLRVD 267
SEQ ID NO: 248 +LGDKIAS+I+AQ T G+PT+ WSGSG+ ++
SEQ ID NO: 249 Sbjct: 23066 SLGDKIASTIIAQTVGVPTVAWSGSGITME 23155

Trehelase

>C23H3

Length = 39,721

Minus Strand HSPs:

Score = 227 (104.5 bits), Expect = 1.0e-95, Sum P(6) = 1.0e-95
Identities = 36/67 (53%), Positives = 51/67 (76%), Frame = -2

SEQ ID NO:250 Query: 2 VIKNLGYMVDNHGFVPNGGRVYVLTQRSQPPLLTMPVYEYMYSTGDLDFVMEILPTLDKEY 61
SEQ ID NO:251 +I N +++++ GFVPNGGRVYVLT RSQPP PMVYEY++T D+ V +++P ++KEY
SEQ ID NO:252 Sbjct:9798 MILNFAHIIETYGFPNGGRVYVLTQRSQPPFAPMVYEYVLTQDIQLVADLIPVIEKEY 9619

SEQ ID NO:250 Query: 62 EFWIKNR 68
SEQ ID NO:251 FW + R
SEQ ID NO:252 Sbjct: 9618 TFWSEER 9598

Score = 182 (83.8 bits), Expect = 1.0e-95, Sum P(6) = 1.0e-95
Identities = 32/92 (34%), Positives = 55/92 (59%), Frame = -2

SEQ ID NO:253 Query: 146 MDSIRTWSIIPADLNAFMCANARILASLYEAGDFKKVKVFEQRYTWAKREMRHLHWN 205
SEQ ID NO:254 + +I T +I+P DLNAF+C N I+ Y++ G+ K + R+T + ++ +
SEQ ID NO:255 Sbjct: 9372 ISTIETTNI VPDNLNAFLCYNMNIMQLFYKLTGNPLKHLEWSSRFTNFPREAF TKVFYVPA 9193

SEQ ID NO:253 Query: 206 DGIWYDYDIELKTHSNQYVYVSNAPLYAKCYD 237
SEQ ID NO:254 WYDY++ TH+ ++ SNAVPL+++CYD
SEQ ID NO:255 Sbjct: 9192 RKGWYDYNLRTLTHNTDFFASNAVPLFSQC YD 9097

Score = 178 (81.9 bits), Expect = 1.0e-95, Sum P(6) = 1.0e-95
Identities = 37/102 (36%), Positives = 55/102 (53%), Frame = -2

SEQ ID NO:256 Query: 246 VHDYLERQGLLK YTKGLPTSLAMSSTQQWDKENAWPPMIH MVIEGFRTTGDIKLMKVAEK 305
SEQ ID NO:257 V++ ++ G G+PTS+ + QQWD N W PM HM+IEG R + + L + A
SEQ ID NO:258 Sbjct: 9069 VYNEMQNSGAFSIPGGIPTSMNEETNQQWDFPNGWSPMNHMIEGLRKSNNPILQQKFT 8890

SEQ ID NO:256 Query: 306 MATSWLTGTYQS FIRTHAMFEKYNVTPHTEETSGGGGG EYEV 347
SEQ ID NO:257 +A WL Q+F + M+EKYNV + + GG E +V
SEQ ID NO:258 Sbjct: 8889 LAEKWLETNMQTFNVSDMWEKYNVKEPLGK LATGGEYEVQV 8764

Score = 169 (77.8 bits), Expect = 1.0e-95, Sum P(6) = 1.0e-95
Identities = 29/58 (50%), Positives = 41/58 (70%), Frame = -2

SEQ ID NO:259 Query: 84 YQYKAKLKVPRPESYREDSELAHLQTEAEKIQMWSEIASAAETGWDFSTRWFSQNGD 141
SEQ ID NO:260 +QY+ + + PRPES+RED AEH T+ K Q + ++ SAAE+GWDFS+RWF + D
SEQ ID NO:261 Sbjct: 9546 FQYRTEAETPRPESFREDVLSAEHFTTKDRKKQFFKDLGSAESGWDFSSRWFKNHKD 9373

Score = 76 (35.0 bits), Expect = 1.0e-95, Sum P(6) = 1.0e-95
Identities = 13/21 (61%), Positives = 15/21 (71%), Frame = -1

SEQ ID NO:262 Query: 348 QTGFGWTNGVILDLLDKYGDQ 368
SEQ ID NO:263 Q GFGWTNG LDL+ Y D+
SEQ ID NO:264 Sbjct: 8722 QAGFGWTNGAALDLIFTYSR 8660

Score = 45 (20.7 bits), Expect = 1.0e-95, Sum P(6) = 1.0e-95
Identities = 10/24 (41%), Positives = 15/24 (62%), Frame = -1

SEQ ID NO:265 Query: 371 SSSTASKFSFSLSNITFVVFI LYI 394
SEQ ID NO:266 +SS++S F +S VF+LYI
SEQ ID NO:267 Sbjct: 8545 TSSSSSTFGYSNITLITVFVLYI 8474

Score = 38 (17.5 bits), Expect = 2.6e-98, Sum P(7) = 2.6e-98
Identities = 7/7 (100%), Positives = 7/7 (100%), Frame = -2

SEQ ID NO:268 Query: 342 GGEYEVQ 348
SEQ ID NO:269 GGEYEVQ
SEQ ID NO:270 Sbjct: 8787 GGEYEVQ 8767

Score = 37 (17.0 bits), Expect = 1.6e-19, Sum P(4) = 1.6e-19
Identities = 8/18 (44%), Positives = 10/18 (55%), Frame = -2

SEQ ID NO:271 Query: 217 KTHSNQYYVSNAPLYAK 234
SEQ ID NO:272 K ++ YYVS P Y K
SEQ ID NO:273 Sbjct: 30345 KFTAHPYYVSRTPPRYHK 30292

>W05E10

Length = 31,273

Minus Strand HSPs:

Score = 224 (103.1 bits), Expect = 7.0e-90, Sum P(7) = 7.0e-90
Identities = 43/67 (64%), Positives = 49/67 (73%), Frame = -1

SEQ ID NO:274 Query: 2 VIKNLGYMVDNHGFVPNGGRVYYLTRSQPPLTPMVYEEYMSTGDLDFVMEILPTLDKEY 61
SEQ ID NO:275 +I+NL MVD +GFVPNGGRVYYL RSQPP L MVYE Y+ T D FV E+LPTL KE
SEQ ID NO:276 Sbjct: 28957MIRNLASMVDKYGFVPNGGRVYYLQRSQPPFLAAMVYELYEATNDKAFVAELLPTLLKEL28778

SEQ ID NO:274 Query: 62 EFWIKNR 68
SEQ ID NO:275 FW + R
SEQ ID NO:276 Sbjct: 28777 NFWNEKR 28757

Score = 192 (88.4 bits), Expect = 7.0e-90, Sum P(7) = 7.0e-90
Identities = 31/84 (36%), Positives = 52/84 (61%), Frame = -3

SEQ ID NO:277 Query: 154 IIPADLNAFMCANARILASLYEIAAGDFKKVKVFEQRYTWAKREMRELHWNEDGIWYDYD 213

SEQ ID NO:278 ++P DLN + C N I + LYE GD K ++F + + ++ + +N TDG WYDY+
SEQ ID NO:279 Sbjct:2842 7VLPVDLNLGLLCWNMDIMEYLYEQIGDTKNSQIFRNKRADFRDVTQNVFYNRDTGTWYDYN 28248

SEQ ID NO:277 Query: 214 IELKTHSNQYYVSNAPPLYAKCYD 237
SEQ ID NO:278 + ++H+ ++Y S AVPL+ CY+
SEQ ID NO:279 Sbjct: 28247 LRTQSHNPRFYTSTAVPLFTNCYN 28176

Score = 125 (57.5 bits), Expect = 7.0e-90, Sum P(7) = 7.0e-90
Identities = 20/48 (41%), Positives = 30/48 (62%), Frame = -2

SEQ ID NO 280 Query: 249 YLERQGLLKYTGLPTSLAMSSTQQWDKENAWPPMIHMOVIEGFRITGD 296
SEQ ID NO 281 + ++ G+ Y G+PTS++ S QQWD N W P HM+IEG R + +
SEQ ID NO 282 Sbjct: 28092 FFQKMGVFTYPPGGIPTSMSQESDQQWDFPNGWSPNNHMIIEGLRKSAN 27949

Score = 90 (41.4 bits), Expect = 7.0e-90, Sum P(7) = 7.0e-90
Identities = 15/18 (83%), Positives = 18/18 (100%), Frame = -2

SEQ ID NO 283 Query: 120 EIASAAETGWDFSTRWFS 137
SEQ ID NO 284 ++ASAAE+GWDFSTRWFS
SEQ ID NO 285 Sbjct: 28566 DLASAAESGWDFSTRWFS 28513

Score = 89 (41.0 bits), Expect = 7.0e-90, Sum P(7) = 7.0e-90
Identities = 18/40 (45%), Positives = 24/40 (60%), Frame = -1

SEQ ID NO 286 Query: 79 KQFPYYQYKAKLKVPRPESYREDSELAEHLQTEAEKIQMW 118
SEQ ID NO 287 K F YQYK VPRPESYR D++ + L A++ Q +
SEQ ID NO 288 Sbjct: 28732 KSFKVYQYKTASNVP RPESYRVDTQNSAKLANGADQQQFY 28613

Score = 77 (35.4 bits), Expect = 7.0e-90, Sum P(7) = 7.0e-90
Identities = 14/21 (66%), Positives = 16/21 (76%), Frame = -3

SEQ ID NO 289 Query: 348 QTGFGWTNGVILDLLDKYGDQ 368
SEQ ID NO 290 Q GFGW+NG ILDLL Y D+
SEQ ID NO 291 Sbjct: 24395 QDGFGWSNGAILDLLLTYNDR 24333

Score = 51 (23.5 bits), Expect = 7.0e-90, Sum P(7) = 7.0e-90
Identities = 11/27 (40%), Positives = 16/27 (59%), Frame = -3

SEQ ID NO 292 Query: 365 YGDQFASSSTASKFSFSLNITFVVFI 391
SEQ ID NO 293 Y FASSS AS FS +++ F + +
SEQ ID NO 294 Sbjct: 2846 YN*PFASSSDASSCPFSTNSVIFSILV 2766

Score = 41 (18.9 bits), Expect = 3.3e-93, Sum P(8) = 3.3e-93
Identities = 7/9 (77%), Positives = 8/9 (88%), Frame = -2

SEQ ID NO 295 Query: 340 GGGGEYEVQ 348
SEQ ID NO 296 G GGEY+VQ
SEQ ID NO 297 Sbjct: 24468 GSGGEYDVQ 24442

Score = 39 (18.0 bits), Expect = 2.0e-37, Sum P(5) = 2.0e-37
Identities = 7/14 (50%), Positives = 8/14 (57%), Frame = -2

SEQ ID NO 298 Query: 221 NQYYVSNAPPLYAK 234
SEQ ID NO 299 N YY+ V LY K
SEQ ID NO 300 Sbjct: 4524 NHYYIIQMVSPLYTK 4483

Score = 38 (17.5 bits), Expect = 4.0e-88, Sum P(7) = 4.0e-88
Identities = 11/30 (36%), Positives = 13/30 (43%), Frame = -1

SEQ ID NO 301 Query: 367 DQFASSTASKFSFSLSNITFVVFIYIFS 396
SEQ ID NO 302 DQF S SKFS + F +FS
SEQ ID NO 303 Sbjct: 7588 DQFVISFICSKFSSKNKKLYFCPSHFSLFS 7499

In the Claims:

1. (Twice Amended) A method for identifying a compound that modulates DAF-18 expression or activity, comprising:

(a) providing a nematode, isolated nematode cell, or isolated mammalian cell expressing a nematode *daf-18* gene; and

(b) contacting said nematode, isolated nematode cell, or isolated mammalian cell with a candidate compound[, an alteration in] to determine the effect of said candidate compound on *daf-18* expression or activity, an alteration in said *daf-18* expression or activity following contact of said nematode, isolated nematode cell, or isolated mammalian cell with said candidate compound identifying said candidate compound as a modulatory compound.

2. (Twice Amended) A method for identifying a compound that modulates PTEN expression or activity, comprising:

(a) providing a nematode or isolated nematode cell comprising a mutation in its endogenous *daf-18* gene;

(b) expressing in said nematode or isolated nematode cell a mammalian PTEN gene; and

(c) contacting said nematode or isolated nematode cell with a candidate compound[, an alteration in] to determine the effect of said candidate compound on PTEN expression or activity, an alteration in said PTEN expression or activity following contact with said candidate compound identifying said candidate compound as a modulatory compound.